IMPROVING THE CATALYTIC ACTIVITY OF ISOPENTENYL PHOSPHATE KINASE THROUGH PROTEIN COEVOLUTION ANALYSIS

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Protein rational design has become more and more popular for protein engineering with the advantage of biological big-data. In this study, we described a method of rational design that is able to identify desired mutants by analyzing the coevolution of protein sequence. We employed this approach to evolve an archaeal isopentenyl phosphate kinase that can convert dimethylallyl alcohol (DMA) into precursor of isoprenoids. By designing 9 point mutations, we improved the catalytic activities of IPK about 8-fold in vitro. After introducing the optimal mutant of IPK into engineered E. coli strain for β-carotenoids production, we found that β-carotenoids production exhibited 97% increase over the starting strain. The process of enzyme optimization presented here could be used to improve the catalytic activities of other enzymes.